

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Prudent, James R.
Hall, Jeff G.
Lyamichev, Victor I.

(ii) TITLE OF INVENTION: Invasive Cleavage Of Nucleic Acids

(iii) NUMBER OF SEQUENCES: 69

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Medlen & Carroll, LLP
(B) STREET: 220 Montgomery Street, Suite 2200
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: United States Of America
(F) ZIP: 94104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/682,853
(B) FILING DATE: 12-JUL-1996

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/599,491
(B) FILING DATE: 24-JAN-1996

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ingolia, Diane E.
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(C) REFERENCE/DOCKET NUMBER: FORS-02564

(x) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGGGA	TGCTGCCCT	CTTGAGCCC	AAGGGCCGGG	TCCTCCTGGT	GGACGCCAC	60
CACCTGGCCT	ACCGCACCTT	CCACGCCCTG	AAGGGCCTCA	CCACCAGCCG	GGGGGAGCCG	120
GTGCAGGCAG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTCAAGGA	GGACGGGGAC	180
GCGGTGATCG	TGGTCTTGA	CGCCAAGGCC	CCCTCCTTCC	GCCACGAGGC	CTACGGGGGG	240
TACAAGGCAGG	GCCGGGCC	CACGCCGGAG	GACTTTCCCC	GGCAACTCGC	CCTCATCAAG	300
GAGCTGGTGG	ACCTCCTGGG	GCTGGCGCGC	CTCGAGGTCC	CGGGCTACGA	GGCGGACGAC	360
GTCCTGGCCA	GCCTGGCAA	GAAGGCGGAA	AAGGAGGGCT	ACGAGGTCCG	CATCCTCACC	420
GCCGACAAAG	ACCTTTACCA	GCTCCTTCC	GACCGCATCC	ACGTCCCTCCA	CCCCGAGGGG	480
TACCTCATCA	CCCCGGCCTG	GCTTGGGAA	AAGTACGGCC	TGAGGCCCCGA	CCAGTGGGCC	540
GAECTACCGGG	CCCTGACCGG	GGACGAGTCC	GACAACTTC	CCGGGGTCAA	GGGCATCGGG	600
GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660
CTGGACCGGC	TGAAGCCC	CATCCGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720
CTCTCCTGGG	ACCTGGCAA	GGTGCACACC	GACCTGCC	TGGAGGTGGA	CTTCGCCAAA	780
AGGCAGGGAGC	CCGACCGGGA	GAGGCTTAGG	GCCTTCTGG	AGAGGCTTGA	GTTTGGCAGC	840
CTCCTCCACG	AGTTCGGC	TCTGGAAAGC	CCCAAGGCC	TGGAGGAGGC	CCCCGGCCC	900
CCGCCGGAAG	GGGCCTCGT	GGGCTTGTG	CTTCCCGCA	AGGAGCCAT	GTGGCCGAT	960
CTTCTGGCCC	TGGCGCCGC	CAGGGGGGC	CGGGTCCACC	GGGCCCCGA	GCCTTATAAA	1020
GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGGG	CTTCTCGCCA	AAGACCTGAG	CGTTCTGGCC	1080
CTGAGGGAAAG	GCCTTGGC	CCCAGCCGGC	GACGACCCCA	TGCTCCTCGC	CTACCTCCTG	1140
GACCCTCCA	ACACCACCCC	CGAGGGGTG	GCCCCGGC	ACGGCGGGGA	GTGGACGGAG	1200
GAGGCGGGGG	AGCGGGCCGC	CCTTCCGAG	AGGCTCTCG	CCAACCTGTG	GGGGAGGCTT	1260
GAGGGGGAGG	AGAGGCTCCT	TTGGCTTAC	CGGGAGGTGG	AGAGGCCCCT	TTCCGCTGTC	1320
CTGGCCCACA	TGGAGGCCAC	GGGGGTGCGC	CTGGACGTGG	CCTATCTCAG	GGCCTTGTCC	1380
CTGGAGGTGG	CCGAGGAGAT	CGCCCGCCTC	GAGGCCGAGG	TCTTCCGCCT	GGCCGCCAC	1440
CCCTTCAACC	TCAACTCCC	GGACCAGCTG	GAAAGGGTCC	TCTTGACGA	GCTAGGGCTT	1500
CCCGCCATCG	GCAAGACGGA	GAAGACCGGC	AAGCGCTCCA	CCAGCGCCGC	CGTCTGGAG	1560
GCCCTCCGCG	AGGCCACCC	CATCGTGGAG	AAGATCCTGC	AGTACCGGGGA	GCTCACCAAG	1620
CTGAAGAGCA	CCTACATTGA	CCCCTTGCGC	GACCTCATCC	ACCCCAGGAC	GGGCCGCCTC	1680
CACACCCGCT	TCAACCAGAC	GGCCACGGCC	ACGGGCAGGC	TAAGTAGCTC	CGATCCAAC	1740
CTCCAGAAC	TCCCCGTCCG	CACCCCGCTT	GGGCAGAGGA	TCCGCCGGGC	CTTCATGCC	1800

GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC	1860
CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCAGG AGGGGCGGGA CATCCACACG	1920
GAGACCGCCA GCTGGATGTT CGGGGTCCCC CGGGAGGCCG TGGACCCCT GATGGGCCGG	1980
GCGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCACCG CCTCTCCCAG	2040
GAGCTAGCCA TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC	2100
CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG	2160
GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG	2220
CGGGAGGCCG CCGAGCGCAT GCCCTTCAAC ATGCCGTCC AGGGCACCGC CGCCGACCTC	2280
ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC	2340
CTTCAGGTCC ACGACGAGCT GGTCTCGAG GCCCCAAAAG AGAGGGCGGA GGCGTGGCC	2400
CGGCTGGCCA AGGAGGTCAAT GGAGGGGGTG TATCCCTGG CCGTGCCCCCT GGAGGTGGAG	2460
GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC	2506

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC TTCCCTCTT TGAGCCAAA GGCGCGTGC TCCTGGTGGA CGGCCACCAC	60
CTGGCCTACC GCACCTCTT TGCCCTCAAG GGCTCACCA CCAGCCGCCG CGAACCCGTT	120
CAGGCGGTCT ACGGCTTCGC CAAAGCCTC CTCAAGGCCG TGAAGGAGGA CGGGGACGTG	180
GTGGTGGTGG TCTTGACGC CAAGGCCCGC TCCTCCGCC ACGAGGCCTA CGAGGCCTAC	240
AAGGCGGGCC GGGCCCCCAC CCCGGAGGAC TTTCCCGGC AGCTGGCCCT CATCAAGGAG	300
TTGGTGGACC TCCTAGGCCT TGTGCGGCTG GAGGTTCCCG GCTTGAGGC GGACGACGTG	360
CTGGCCACCC TGGCCAAGCG GGCGGAAAAG GAGGGTAGC AGGTGCGCAT CCTCACTGCC	420
GACCGCGACC TCTACCAGCT CCTTTCGGAG CGCATGCCA TCCTCCACCC TGAGGGTAC	480
CTGATCACCC CGCGTGGCT TTACGAGAAG TACGGCTGC GCCCGGAGCA GTGGGTGGAC	540
TACCGGGCCC TGGCGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGAG	600
AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG	660
GACCAGGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCCG GCATGGAGGC CCTGGCCCTT	720
TCCCGGAAGC TTTCCCAGGT GCACACTGAC CTGCCCTGG AGGTGGACTT CGGGAGGCCG	780

CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTGGAGC GGTTGGAGTT TGGAAGCCTC	840
CTCCACGAGT TCGGCCTCCT GGAGGGGCCG AAGGCGGCAG AGGAGGCCCC CTGGCCCCCT	900
CCGGAAGGGG CTTTTTGGG CTTTCCTTT TCCCCTCCCG AGCCCATGTG GGCCGAGCTT	960
CTGGCCCTGG CTGGGGCGTG GGAGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGC	1020
CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG	1080
CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC	1140
CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCCTTACG GGGGGGAGTG GACGGAGGAT	1200
GCGGGGGAGA GGGCCCTCCT GGCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG	1260
GGAGAAGAAC GCCTGCTTG GCTTACGAG GAGGTGGAGA AGCCGCTTC CGGGTGTG	1320
GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG	1380
GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCC	1440
TTCAACCTCA ACTCCCGCA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT	1500
GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC	1560
CTGCGAGAGG CCCACCCAT CGTGGACCAG ATCCTGCAGT ACCGGGAGCT CACCAAGCTC	1620
AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CGGGCTCCAC	1680
ACCCGTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCAACCTG	1740
CAGAACATCC CCGTGCAC CCCTCTGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG	1800
GAGGGCTGGG TGCTGGGGT CTTGGACTAC AGCCAGATTG AGCTTGGGT CCTGGCCAC	1860
CTCTCCGGGG ACGAGAACCT GATCCGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG	1920
ACGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGTAG ACCCTCTGAT GCGCCGGGG	1980
GCCAAGACCA TCAAATTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGAG	2040
CTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCC	2100
AAGGTGCGGG CCTGGATTGA GGGGACCTC GAGGAGGGCC GCCGGGGGG GTATGTGGAG	2160
ACCCTCTTCG GCCGCCGGCG CTATGTGCC GACCTCAACG CCCGGGTGAA GAGCGTGC	2220
GAGGCAGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG	2280
AAGCTGGCCA TGGTGGGGT TTTCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTG	2340
CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT	2400
TTGGCCAAGG AGGTCACTGGA GGGGGTCTGG CCCCTGCAGG TGCCCTGGA GGTGGAGGTG	2460
GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG	2496

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGC	GA TGCTTCCG	CCTTGAA	CC AAAGGCC	GGG TCCTC	TGGT GGACGCC	AC	60
CACCTGG	CCT ACCGCAC	CTT CGCC	CTG AAGGC	CCTCA CCACGAG	CCG GGGCGA	ACCG	120
GTGCAGG	CGG TCTACGG	CTT CGCAAG	AGC CTCCTAAG	GG CCCTGA	AAGGA GGACGG	TAC	180
AAGGCCG	TCT TGCGT	CTT TGACGCC	AAAG GCCCC	CTT TCCGCC	ACGA GGC	CTACGAG	240
GCCTACA	AGG CGGCT	CCG CCGAAC	CCC GAGACT	CCCG CAGCT	CGCC	CTCATC	300
AAGGAGC	TGG AGCTGG	CCG GGGAC	CTT CGGAGG	CTT CGGAGG	CGAGG C	GCGAC	360
GACGTTCT	CG CCACCTGG	CAAGAAGG	CG GAAAAGG	AGG GGTAC	GAGG G	TACGAG	420
ACCGCCG	ACC GCGAC	CTTA CGCT	CCGACCG	CG TCGCC	GGTCC	CGGAC	480
GGCCAC	CTCA CCCCG	GA GTGGCTT	GGG GAGTAC	GCCTCAGG	CC GGAG	CAGTGG	540
GTGGACTT	CCG GCGCC	CTG GGGGAC	CCC TCCGACA	ACCG TCCC	CGGGG	GGGAGT	600
GGGGAGA	AGA ACGCCTCA	GG GCTCCT	CTAAG GAGT	GGGAA GCCTG	GGGAAAA	CTCCTCA	660
AACCTGG	ACC GGGTAA	AGG AGC	GGGAGAAGA	GGG TCAAGG	CCGCCA	GGAAAGAC	720
CTCAGG	CTCT GGAGCT	CTCC CGGTG	CGC ACCG	ACCC CGTGA	GGTGG	ACCTC	780
GCCCAGG	GGG GAGCC	GA CCGGG	CTTAGGGC	CTC TGGAGA	GGTGGAG	GTTC	840
GGCAGC	CTCC ACAGT	CGGC CCTCG	GA GGGCCCC	CG CCCCC	GGAGG	CCCCG	900
TGGCCCC	CG GAAGGG	CTTC GTGGG	CTCG TCC	CTC CGCC	GGCC ATGT	GG	960
CGGGAGCT	TA AGCC	CGC CTG CAG	GA CGGCC	GG TGCA	CGGGG	ACCCCC	1020
TTGGCGGG	CTAA AGGAC	CTA AGGAG	GC GGGCC	CTC CAAGG	GGG GAC	CTCGCC	1080
TTGGCCTC	GA GGGGGCT	AG ACCTCG	CCC GGGAC	ACCC CATG	GGG GAGT	GG	1140
CTCCTGG	ACCG GAGGAC	CC CCAACAC	CA CCCCCG	GGGG TGGCG	GGCG CTACGG	GGGGAGT	1200
ACGGAGG	ACG CCGCC	ACCG GGGAC	GGG TGGAGG	GC TCCATG	GGGGAGT	GG	1260
CGCCTCG	AGG GAGGAG	GA GCTC	CTT TTGG	CTCT ACCAC	AG GTGG	AAAA GCCC	1320
CGGGTCC	GGG GAGGAG	GGC CACCG	GGG GTGGCG	GTACGGCT	ACGTGGC	CTA CCTTCAGGCC	1380
CTTTCC	GGG GAGGAG	GGG GAGATCC	GGG GAGATCC	CGC CTGAGG	AGG AGGT	CTT CCGCTT	1440
GGCCACCC	CTCA ACCTCA	CTCCC	GGG GAGGAC	CA GCTGGAAA	GGGTG	CTT TGCG	1500

AGGCTTCCCG CCTTGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG	1560
CTGGAGGCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC	1620
ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC	1680
CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC	1740
CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CGGGGCCTTC	1800
GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC	1860
CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC	1920
CACACCCAGA CCGCAAGCTG GATGTTCGGC GTCCCCCGG AGGCCGTGGA CCCCTGATG	1980
CGCCGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC	2040
TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA	2100
GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT	2160
ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA	2220
GCGTCAGGGA GGCGCGGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG	2280
ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCCGCCT CCGGGAGATG GGGGCCCGCA	2340
TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG	2400
TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG	2460
TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG	2504

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 832 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
50 55 60

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
65 70 75 80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
 85 90 95
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
 100 105 110
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
 115 120 125
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
 130 135 140
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
 145 150 155 160
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175
 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
 180 185 190
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
 195 200 205
 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
 210 215 220
 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
 225 230 235 240
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
 325 330 335
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
 405 410 415

Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
 420 425 430
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 770 775 780
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
 785 790 795 800
 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
 820 825 830

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
 1 5 10 15
 Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
 20 25 30
 Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
 35 40 45
 Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val
 50 55 60
 Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
 65 70 75 80
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95
 Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
 100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
 130 135 140
 Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
 165 170 175
 Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
 180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
 195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
 210 215 220
 Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu
 225 230 235 240
 Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu
 260 265 270
 Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu
 275 280 285
 Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
 290 295 300
 Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
 305 310 315 320
 Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp
 325 330 335
 Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala
 340 345 350
 Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro
 355 360 365
 Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
 370 375 380
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
 385 390 395 400
 Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys
 405 410 415
 Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val
 420 425 430
 Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val
 435 440 445
 Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala
 450 455 460
 Glu Val Arg Gln Leu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495
 Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser
 500 505 510
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 515 520 525

Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
 530 535 540
 Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His
 545 550 555 560
 Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
 565 570 575
 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
 580 585 590
 Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Val Leu Val Val Leu
 595 600 605
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 610 615 620
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln
 625 630 635 640
 Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu
 645 650 655
 Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
 660 665 670
 Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala
 675 680 685
 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala
 690 695 700
 Trp Ile Glu Gly Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu
 705 710 715 720
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
 725 730 735
 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
 740 745 750
 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe
 755 760 765
 Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp
 770 775 780
 Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala
 785 790 795 800
 Leu Ala Lys Glu Val Met Glu Gly Val Trp Pro Leu Gln Val Pro Leu
 805 810 815
 Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu
 820 825 830

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
225 230 235 240

Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
245 250 255

Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGNNGGCGA TGCTTCCCCT CTTTGAGCCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACCAGCCG GGGCGAACCG	120
GTCAGGCAGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGGAC	180

NNGGCGGTGN TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGCCGGGC CCCCACCCCG GAGGACTTTC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTTGCG CGCCTCGAGG TCCCCGGCTA CGAGGGGGAC	360
GACGTNCTGG CCACCCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC	420
ACCGCCGACC GCGACCTCTA CCAGCTCCTT TCCGACCGCA TCGCCGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCAGC GTGGCTTTGG GAGAAGTACG GCCTGAGGCC GGAGCAGTGG	540
GTGGACTACC GGGCCCTGGC GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCNAGA GCTCCTCNAG GAGTGGGGGA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTGAAGCC CGCCNTCCGG GAGAAGATCC AGGCCCACAT GGANGACCTG	720
ANGCTCTCCT GGGAGCTNTC CCAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAGNGGCGGG AGCCCGACCG GGAGGGGCTT AGGGCCTTTC TGGAGAGGCT GGAGTTGGC	840
AGCCTCTCCT ACAGAGTCGG CCTCCTGGAG GGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTCCTTCCC GCCCGAGCC CATGTGGGCC	960
GAGCTCTGG CCCTGGCCGC CGCCAGGGAG GGCCGGGTCC ACCGGGCACC AGACCCCTTT	1020
ANGGGCCTNA GGGACCTNA GGAGGTGCGG GGNCTCTCG CCAAGGACCT GGCGTTTG	1080
GCCCTGAGGG AGGGCCTNGA CCTCNTGCC CGGGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCCT CCAACACCAC CCCGAGGGG GTGGCCCGGC GCTACGGGG GGAGTGGACG	1200
GAGGANGCGG GGGAGCGGGC CCTCCTNTCC GAGAGGCTCT TCCNGAACCT NNNGCAGCGC	1260
CTTGAGGGGG AGGAGAGGCT CCTTGCGTT TACCAAGGAGG TGGAGAAGCC CCTTTCCGG	1320
GTCCTGGCCC ACATGGAGGC CACGGGGTN CGGCTGGACG TGGCCTACCT CCAGGCCCTN	1380
TCCCTGGAGG TGGCGGAGGA GATCCGCCGC CTCGAGGAGG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TGCTCTTGA CGAGCTNGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACN GGCAAGCGCT CCACCAGCGC CGCCGTGCTG	1560
GAGGCCCTNC GNGAGGCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCAC	1620
AAGCTCAAGA ACACCTACAT NGACCCCTG CCNGNCCTCG TCCACCCAG GACGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGCA GGCTTAGTAG CTCCGACCCC	1740
AACCTGCAGA ACATCCCCGT CCGCACCCCN CTGGGCCAGA GGATCCGCCG GGCCTCGTG	1800
GCCGAGGAGG GNTGGGTGTT GGTGGCCCTG GACTATAGCC AGATAGAGCT CCGGGTCCTG	1860
GCCCCACCTCT CCGGGGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGAG GGACATCCAC	1920
ACCCAGACCG CCAGCTGGAT GTTCGGCGTC CCCCCGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATAA CTTGGGGTC CTCTACGGCA TGTCCGCCA CGCCTCTCC	2040

CAGGAGCTTG CCATCCCCTA CGAGGAGGCG GTGGCCTTCA TTGAGCGCTA CTTCCAGAGC	2100
TTCCCCAAGG TGCAGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC	2160
GTGGAGACCC TCTTCGGCCG CCGCGCTAC GTGCCGACC TCAACGCCCG GGTGAAGAGC	2220
GTGCGGGAGG CGGCGGAGCG CATGGCCTTC AACATGCCCG TCCAGGGCAC CGCCGCCGAC	2280
CTCATGAAGC TGGCCATGGT GAAGCTCTTC CCCCGGCTNC AGGAAATGGG GGCCAGGATG	2340
CTCCTNCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCA AAGAGCGGGC GGAGGNGGTG	2400
GCCGCTTGG CCAAGGAGGT CATGGAGGGG GTCTATCCCC TGGCCGTGCC CCTGGAGGTG	2460
GAGGTGGGGA TGGGGGAGGA CTGGCTCTCC GCCAAGGAGT AG	2502

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 833 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu			
1	5	10	15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly			
20	25	30	
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala			
35	40	45	
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val			
50	55	60	
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala			
65	70	75	80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu			
85	90	95	
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu			
100	105	110	
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys			
115	120	125	
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp			
130	135	140	
Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly			
145	150	155	160
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro			
165	170	175	

Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
 180 185 190
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu
 195 200 205
 Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val
 210 215 220
 Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa
 225 230 235 240
 Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa
 325 330 335
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu
 405 410 415
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 770 775 780
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu
 820 825 830

Xaa

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1647 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCTGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CGGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCAGGCTA CGAGGCGGAC	360
GACGTCTGG CCAGCCTGGC CAAGAACGGCG GAAAAGGAGG GCTACGAGGT CCGCATTCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAACATCC TGGCCCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCCG ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTGGC	840
AGCCTCCTCC ACGAGTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGCCTT CGTGGGCTTT GTGCTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCG CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTCTCG CCAAAGACCT GAGCCTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGTCCT CGCCTACCTC	1140
CTGGACCCCTT CCAACACCAAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAAG CTGGAAAGGG TCCTCTTGA CGAGCTAGGG	1500

CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCTG	1560
GAGGCCCTCC GCGAGGCCA CCCCCATCGTG GAGAAGATCC TGCAGGCATG CAAGCTTGGC	1620
ACTGGCCGTC GTTTACAAC GTCGTGA	1647

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAATTCCGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTGG CCAGCCTGGC CAAGAAGGGC GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGCCTT CGTGGCTTT GTGCTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGTCC ACCGGGCCCC CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGGG GGGCTTCTCG CCAAAGACCT GAGCCTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCCTT CCAACACCAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTCCGCT	1320

GTCCCTGGCCC ACATGGAGGC CACGGGGTG CGCCTGGACG TGGCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CGGGGACCA CTGGAAAGGG TCCTCTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCCA CCCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCAC	1620
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGCA GGCTAAGTAG CTCCGATCCC	1740
AACCTCCAGA ACATCCCCGT CCGCACCCCCG CTTGGCAGA GGATCCGCCG GGCTTCATC	1800
GCCGAGGAGG GGTGGCTATT GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG	1860
GCCCACCTCT CCGGCGACGA GAACCTGATC CGGGTCTTCC AGGAGGGCG GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCAGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA CTTGGGTC CTCTACGGCA TGTCGGCCA CCGCCTCTCC	2040
CAGGAGCTAG CTAGCCATCC CTTACGAGGA GGCCCAGGCC TTCATTGA	2088

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCTGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCAACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CGGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTGCCAAG AGCCTCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCTACGGG	240
GGGTACAAGG CGGGCCGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CGCATCCTC	420
ACCGCCGACA AAGACCTTA CCAGCTTCTT TCCGACCGCA TCCACGTCCT CCACCCGAG	480
GGGTACCTCA TCACCCGGC CTGGCTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720

AAGCTCTCCT	GGGACCTGGC	CAAGGTGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTGGC	840
AGCCTCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGT	CATGGAGGGG	GTGTATCCCC	900
TGGCCGTGCC	CCTGGAGGTG	GAGGTGGGG	TAGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	960
GA						962

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAATT	CG GGGATGCTGC	CCCTCTTG	GA GCCCAAGGGC	CGGGTCCTCC	TGGTGGACGG	60
CCACCACCTG	GCCTACCGCA	CCTTCCACGC	CCTGAAGGGC	CTCACCA	GCCGGGGG	120
GCCGGTGCAG	GCGGTCTACG	GCTTCGCCAA	GAGCCTCCTC	AAGGCCCTCA	AGGAGGACGG	180
GGACGCGGTG	ATCGTGGTCT	TTGACGCCAA	GGCCCCCTCC	TTCCGCCACG	AGGCCTACGG	240
GGGGTACAAG	GCGGGCCGGG	CCCCCACGCC	GGAGGACTTT	CCCCGGCAAC	TCGCCCTCAT	300
CAAGGAGCTG	GTGGACCTCC	TGGGGCTGGC	GCGCCTCGAG	GTCCCGGGCT	ACGAGGCGGA	360
CGACGTCTG	GCCAGCCTGG	CCAAGAACGC	GGAAAAGGAG	GGCTACGAGG	TCCGCATCCT	420
CACCGCCGAC	AAAGACCTTT	ACCAGCTCCT	TTCCGACC	GC ATCCACGTCC	TCCACCCGA	480
GGGGTACCTC	ATCACCCCGG	CCTGGCTTTG	GGAAAAGTAC	GGCCTGAGGC	CCGACCAGTG	540
GGCCGACTAC	CGGGCCCTGA	CCGGGGACGA	GTCCGACAAC	CTTCCC	GGGG TCAAGGGCAT	600
CGGGGAGAAG	ACGGCGAGGA	AGCTTCTGGA	GGAGTGGGGG	AGCCTGGAAG	CCCTCCTCAA	660
GAACCTGGAC	CGGCTGAAGC	CCGCCATCCG	GGAGAAGATC	CTGGCCCACA	TGGACCGATCT	720
GAAGCTCTCC	TGGGACCTGG	CCAAGGTGCG	CACCGACCTG	CCCCTGGAGG	TGGACTTCGC	780
CAAAGGCCG	GAGCCGACC	GGGAGAGGCT	TAGGGCTTT	CTGGAGAGGC	TTGAGTTGG	840
CAGCCTCCTC	CACGAGTTG	GCCTTCTGGA	AAGCCCCAAG	ATCCGCCGGG	CCTTCATCGC	900
CGAGGAGGGG	TGGCTATTGG	TGGCCCTGGA	CTATAGCCAG	ATAGAGCTCA	GGGTGCTGGC	960
CCACCTCTCC	GGCGACGAGA	ACCTGATCCG	GGTCTCCAG	GAGGGGGCGGG	ACATCCACAC	1020
GGAGACCGCC	AGCTGGATGT	TGGGGCTCCC	CCGGGAGGCC	GTGGACCCCC	TGATGGGCCG	1080
GGCGGCCAAG	ACCATCAACT	TCGGGGCTCT	CTACGGCATG	TCGGCCCACC	GCCTCTCCCA	1140
GGAGCTAGCC	ATCCCTTACG	AGGAGGCCA	GGCCTCATT	GAGCGCTACT	TTCAGAGCTT	1200

CCCCAAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC GGGGGTACGT	1260
GGAGACCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA GAGGCCCGGG TGAAGAGCGT	1320
GCGGGAGGCG GCGGAGCGCA TGGCCTTCAA CATGCCCGTC CGGGGCACCG CCGCCGACCT	1380
CATGAAGCTG GCTATGGTGA AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT	1440
CCTTCAGGTC CACGACGAGC TGGTCCTCGA GGCCCCAAA GAGAGGGCGG AGGCCGTGGC	1500
CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCCTG GCCGTGCCCG TGGAGGTGGA	1560
GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA	1600

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCTG GGGATGCTGC CCCTCTTGA GCCCAA	36
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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC	34
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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CGGGCGAGC TCGAATTCCG	60
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TGTATTCTAT AGTGTACCT AAATCGAATT C	91
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(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC 30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTCTGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGGGGAC	360
GACGTCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCG CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTCTCG CCAAAGACCT GAGCGTTCTG	1080

GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCCTT CCAACACCAAC CCCCGAGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCCG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTCTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCA CCCCATCGTG GAGAAGATCC TGCACTACCG GGAGCTCAC	1620
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGCA GGCTAAGTAG CTCCGATCCC	1740
AACCTCCAGA ACATCCCCGT CCGCACCCCG CTTGGCAGA GGATCCGCCG GGCCTTCATC	1800
GCCGAGGAGG GGTGGCTATT GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG	1860
GCCCACCTCT CCGCGACGA GAACCTGATC CGGGTCTTCC AGGAGGGCGG GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCAGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATAA CTTGGGGTC CTCTACGGCA TGTGGCCCA CGCCCTCTCC	2040
CAGGAGCTAG CCATCCCTTA CGAGGAGGCC CAGGCCCTCA TTGAGCGCTA CTTTCAGAGC	2100
TTCCCAAGG TGCGGGCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC	2160
GTGGAGACCC TCTTCGGCCG CCGCCGCTAC GTGCCAGACC TAGAGGCCCG GGTGAAGAGC	2220
GTGCGGGAGG CGGCCGAGCG CATGGCCTTC AACATGCCG TCCGGGGCAC CGCCGCCGAC	2280
CTCATGAAGC TGGCTATGGT GAAGCTCTTC CCCAGGCTGG AGGAAATGGG GGCCAGGATG	2340
CTCCTTCAGG TCCACGACGA GCTGGCCTC GAGGCCCAA AAGAGAGGCC GGAGGCCGTG	2400
GCCCGGCTGG CCAAGGAGGT CATGGAGGGG GTGTATCCCC TGGCCGTGCC CCTGGAGGTG	2460
GAGGTGGGAGA TAGGGAGGA CTGGCTCTCC GCCAAGGAGT GA	2502

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTAGGTG ACACTATAG

19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA	60
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CACAGCAGAA AC	72
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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTTCTGCTG TGTGCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG	60
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CTTGTTCGTC	70
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(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG	20
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(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTGCGTCTCT CTTG	24
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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGTAC CATGTTGATC CTGTGTCGCT GTCTCGCTTG TTTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGAAG AGAGACGACA CAGCAGAAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Ile	Asn	Ser
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCCGGGAT GCTGCCCTC

60

TTTGAGCCA AGGGCCGGGT CCTCCTGGTG GACGCCACC ACCTGGCCTA CCGCACCTTC

120

CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC

180

GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTGAC

240

GCCAAGGCC	CCTCCTCCG	CCACGAGGCC	TACGGGGGT	ACAAGGCGGG	CCGGGCC	300
ACGCCGGAGG	ACTTCCCCG	GCAACTCGCC	CTCATCAAGG	AGCTGGTGG	CCTCCTGGG	360
CTGGCGGCC	TCGAGGTCCC	GGGCTACGAG	GCGGACGACG	TCCTGGCCAG	CCTGGCCAAG	420
AAGGC GGAAA	AGGAGGGCTA	CGAGGTCCGC	ATCCTCACCG	CCGACAAAGA	CCTTTACCAG	480
CTTCTTCCG	ACCGCATCCA	CGTCCTCCAC	CCCGAGGGGT	ACCTCATCAC	CCCGGCC	540
CTTTGGAAA	AGTACGGCCT	GAGGCCGAC	CAGTGGCCG	ACTACCGGGC	CCTGACCGGG	600
GACGAGTCCG	ACAACCTTCC	CGGGGTCAAG	GGCATCGGGG	AGAACGACGGC	GAGGAAGCTT	660
CTGGAGGAGT	GGGGGAGCCT	GGAAGCCCTC	CTCAAGAAC	TGGACCGGCT	GAAGCCGCC	720
ATCCGGAGA	AGATCCTGGC	CCACATGGAC	GATCTGAAGC	TCTCCTGGGA	CCTGGCCAAG	780
GTGCGCACCG	ACCTGCCCCT	GGAGGTGGAC	TTGCCAAAA	GGCGGGAGCC	CGACCGGGAG	840
AGGCTTAGGG	CCTTTCTGGA	GAGGCTTGAG	TTTGGCAGCC	TCCTCCACGA	GTTCGGCCTT	900
CTGGAAAGCC	CCAAGTCATG	GAGGGGGTGT	ATCCCCTGGC	CGTCCCCCTG	GAGGTGGAGG	960
TGGGGATAG						969

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 948 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA	TGACTGGTGG	ACAGCAAATG	GGTCGGATCA	ATTGGGGAT	GCTGCCCTC	60
TTTGAGCCA	AGGGCCGGT	CCTCCTGGTG	GACGCCACC	ACCTGGCCTA	CCGCACCTTC	120
CACGCCCTGA	AGGGCCTAC	CACCAGCCGG	GGGGAGCCGG	TGCAGGCGGT	CTACGGCTTC	180
GCCAAGAGCC	TCCTCAAGGC	CCTCAAGGAG	GACGGGGACG	CGGTGATCGT	GGTCTTGAC	240
GCCAAGGCC	CCTCCTTCCG	CCACGAGGCC	TACGGGGGT	ACAAGGCGGG	CCGGGCC	300
ACGCCGGAGG	ACTTCCCCG	GCAACTCGCC	CTCATCAAGG	AGCTGGTGG	CCTCCTGGG	360
CTGGCGGCC	TCGAGGTCCC	GGGCTACGAG	GCGGACGACG	TCCTGGCCAG	CCTGGCCAAG	420
AAGGC GGAAA	AGGAGGGCTA	CGAGGTCCGC	ATCCTCACCG	CCGACAAAGA	CCTTTACCAG	480
CTTCTTCCG	ACCGCATCCA	CGTCCTCCAC	CCCGAGGGGT	ACCTCATCAC	CCCGGCC	540
CTTTGGAAA	AGTACGGCCT	GAGGCCGAC	CAGTGGCCG	ACTACCGGGC	CCTGACCGGG	600
GACGAGTCCG	ACAACCTTCC	CGGGGTCAAG	GGCATCGGGG	AGAACGACGGC	GAGGAAGCTT	660
CTGGAGGAGT	GGGGGAGCCT	GGAAGCCCTC	CTCAAGAAC	TGGACCGGCT	GAAGCCGCC	720

ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG	780
GTGCGCACCG ACCTGCCCT GGAGGTGGAC TTCGCCAAA GGCGGGAGCC CGACCAGGAG	840
AGGCTTAGGG CCTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT	900
CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCAAC ACCACTGA	948

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTTC TCTGCTCTCT GGTCGCTGTC TCGCTGTTC GTC	43
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(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTCGTC	19
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(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCTGGGTTC TCTGCTCT GGTC

24

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA

43

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGCTATG ACCATGATTA C

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTTCTCTGCT CTCTGGTCGC TGTCTCGCTT GTGAAACAAG CGAGACAGCG TGGTCTCTCG

60

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGAGAGACCA CGCTG

15

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTGCCG GCTTTCCCCG TC

52

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGAAAGGAAG GGAAGAAAGC GAAAGG

26

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GACGGGGAAA GCCGGCGAAC G

21

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAAAGCCGGC GAACGTGGCG

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGCGAACGTG GCGAGAAAGG A

21

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCTTTCGCTT TCTTCCCTTC CT TTCTCGCC AC GTT CGCCG GC

42

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CCTTTCGCTC TCTTCCCTTC CT TTCTCGCC AC GTT CGCCG GC

42

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 8
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/mod_base= OTHER

/note= "The A residue at this position is 2'-O-methyladenosine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGAAAGGAAG GGAAGAAC GAAAGGT

27

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCGGCGAAC GTGGCGAGAA AGGA

24

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTTTCTT TGAGGTTTAG

20

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCGACACTCC ACCATAGAT

19

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTGTCTTCAC GCAGAAAGC

19

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCACGGTCTA CGAGACCTC

19

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGAAAGCUU GCAUGCCUGC AGGUCGACUC UAGAGGAUCU ACUAGUCAUA UGGAUUCUGU	60
CUUCACCGAG AAAGCGUCUG GCCAUGGCUG UAGUAUGAGU GUCGUGCAGC CUCCAGGACC	120
CCCCCUCCCG GGAGAGGCAU AGUGGUUCUGC GGAACCGGUG AGUACACCGG AAUUGCCAGG	180
ACGACCGGGU CCUUUCUUGG AUAAACCCGC UCAAUGCCUG GAGAUUUGGG CGUGCCCCCG	240
CAAGACUGCU AGCCGAGUAG UGUUGGGUCG CGAAAGGCCU UGUGGUACUG CCUGAUAGGG	300
UGCCUGCGAG UGCCCGGGGA GGUCUCGUAG ACCGUGC	337

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 18
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/note= "The N at this position indicates the presence of a fluorescein dye on an abasic linker."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGTCGTCC TGGCAATNCC

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GTTTATCCAA GAAAGGACCC GGTCC

25

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CAGGGTGAAAG GGAAGAAGAA AGCGAAAGGT

30

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CAGGGGGAAG GGAAGAAGAA AGCGAAAGGT

30

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 1..2
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/mod_base= OTHER

/note= "The T residues at positions 1 and 2 are amino modified T residues."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
 TTCTTTCAC CAGCGAGACG GG 22

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
 ATTGGGCGCC AGGGTGGTTT TT 22

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
 CCCGTCTCGC TGGTGAAAAG AAAAACCAAC CTGGCGCCA ATACGCAAAC CGC 53

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
 GAATTCGATT TAGGTGACAC TATAGAATAAC A 31

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
 CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GC 42

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCCCCGCGAAC GTGGCGAGAA AGGA

24

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAGAAGGAAG GGAAGAAAGC GAAAGG

26

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CAGGGGGAAG GGAAGAAAGC GAAAGG

26

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGGGTACAG GGAAGAAAGC GAAAGG

26